

*Re-ref*

1600

## RAW SEQUENCE LISTING

DATE: 09/08/2004

PATENT APPLICATION: US/09/857,583B

TIME: 12:37:13

Input Set : N:\Crf4\Refhold\09\_folder\I857583B.raw

Output Set: N:\CRF4\09082004\I857583B.raw

C--> 1 <110> APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION  
 2 Browse, John A  
 3 Wallis, James G  
 4 Watts, Jennifer L.  
 5 <120> TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF  
 6 POLYUNSATURATED FATTY ACIDS  
 7 <130> FILE REFERENCE: 4630-58963  
 8 <140> CURRENT APPLICATION NUMBER: US/09/857,583B  
 9 <141> CURRENT FILING DATE: 2001-08-17  
 10 <150> PRIOR APPLICATION NUMBER: US 60/111,301  
 11 <151> PRIOR FILING DATE: 1998-12-07  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US99/28655  
 13 <151> PRIOR FILING DATE: 1999-12-06  
 14 <160> NUMBER OF SEQ ID NOS: 16  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1461  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Caenorhabditis elegans  
 21 <400> SEQUENCE: 1

22	gaattttcaa	tcctccttgg	gtcccaccgc	tgtgatatca	aaatggtatt	acgagagcaa	60
23	gagcatgagc	cattcttcat	taaaattgat	ggaaaatggt	gtcaaattga	cgatgctgtc	120
24	ctgagatcac	atccaggtgg	tagtgcaatt	actacctata	aaaatatgga	tgccactacc	180
25	gtattccaca	cattccatac	tggttctaaa	gaagcgtatc	aatggctgac	agaattgaaa	240
26	aaagagtgcc	ctacacaaga	accagagatc	ccagatatta	aggatgaccc	aatcaaaagga	300
27	attgatgatg	tgaacatggg	aactttcaat	atttctgaga	aacgatctgc	ccaaataaat	360
28	aaaagtttca	ctgatctacg	tatgcgagtt	cgtgcagaag	gacttatgga	tggatctcct	420
29	ttgttctaca	ttagaaaaat	tcttgaaaca	atcttcacaa	ttctttttgc	attctacctt	480
30	caataccaca	catattatct	tccatcagct	attctaattg	gagttgctg	gcaacaattg	540
31	ggatggttaa	tccatgaatt	cgcacatcat	cagttgttca	aaaacagata	ctacaatgat	600
32	ttggccagct	atttcgttgg	aaacttttta	caaggattct	catctggtgg	ttggaaagag	660
33	cagcacaatg	tgcatacgc	agccacaaat	gttgttgga	gagacggaga	tcttgattta	720
34	gtcccattct	atgctacagt	ggcagaacat	ctcaacaatt	attctcagga	ttcatgggtt	780
35	atgactctat	tcagatggca	acatgttcat	tggacattca	tgttaccatt	cctccgtctc	840
36	tcgtggcttc	ttcagtcaat	catttttgtt	agtcagatgc	caactcatta	ttatgactat	900
37	tacagaaata	ctgcgattta	tgaacaggtt	ggtctctctt	tgcactgggc	ttggtcattg	960
38	ggtcaattgt	atttctacc	cgattggtca	actagaataa	tgttcttcct	tgtttctcat	1020
39	cttggtggag	gtttcctgct	ctctcatgta	gttactttca	atcattattc	agtggagaag	1080
40	tttgcatgga	gctcgaacat	catgtcaaat	tacgcttgct	ttcaaatcat	gaccacaaga	1140
41	aatatgagac	ctggaagatt	cattgactgg	ctttggggag	gtcttaacta	tcagattgag	1200
42	caccatcttt	tcccaacgat	gccacgacac	aacttgaaca	ctgttatgcc	acttgtaag	1260
43	gagtttcag	cagcaaatgg	tttaccatac	atggtcgacg	attatttcac	aggattctgg	1320
44	cttgaaattg	agcaattccg	aaatattgca	aatgttgctg	ctaaattgac	taaaaagatt	1380



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45      gcctagatta cgattaatta atcaatttat tttcatgttc tattcgtgtg ttttaatat 1440
46      ttccaaattt ttacctattc c 1461
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 447
50 <212> TYPE: PRT
51 <213> ORGANISM: Caenorhabditis elegans
52 <400> SEQUENCE: 2
53      Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp
54      1 5 10 15
55      Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly
56      20 25 30
57      Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe
58      35 40 45
59      His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu
60      50 55 60
61      Leu Lys Lys Glu Cys Pro Thr Gln Glu Pro Glu Ile Pro Asp Ile Lys
62      65 70 75 80
63      Asp Asp Pro Ile Lys Gly Ile Asp Asp Val Asn Met Gly Thr Phe Asn
64      85 90 95
65      Ile Ser Glu Lys Arg Ser Ala Gln Ile Asn Lys Ser Phe Thr Asp Leu
66      100 105 110
67      Arg Met Arg Val Arg Ala Glu Gly Leu Met Asp Gly Ser Pro Leu Phe
68      115 120 125
69      Tyr Ile Arg Lys Ile Leu Glu Thr Ile Phe Thr Ile Leu Phe Ala Phe
70      130 135 140
71      Tyr Leu Gln Tyr His Thr Tyr Tyr Leu Pro Ser Ala Ile Leu Met Gly
72      145 150 155 160
73      Val Ala Trp Gln Gln Leu Gly Trp Leu Ile His Glu Phe Ala His His
74      165 170 175
75      Gln Leu Phe Lys Asn Arg Tyr Tyr Asn Asp Leu Ala Ser Tyr Phe Val
76      180 185 190
77      Gly Asn Phe Leu Gln Gly Phe Ser Ser Gly Gly Trp Lys Glu Gln His
78      195 200 205
79      Asn Val His His Ala Ala Thr Asn Val Val Gly Arg Asp Gly Asp Leu
80      210 215 220
81      Asp Leu Val Pro Phe Tyr Ala Thr Val Ala Glu His Leu Asn Asn Tyr
82      225 230 235 240
83      Ser Gln Asp Ser Trp Val Met Thr Leu Phe Arg Trp Gln His Val His
84      245 250 255
85      Trp Thr Phe Met Leu Pro Phe Leu Arg Leu Ser Trp Leu Leu Gln Ser
86      260 265 270
87      Ile Ile Phe Val Ser Gln Met Pro Thr His Tyr Tyr Asp Tyr Tyr Arg
88      275 280 285
89      Asn Thr Ala Ile Tyr Glu Gln Val Gly Leu Ser Leu His Trp Ala Trp
90      290 295 300
91      Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met
92      305 310 315 320
93      Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val
94      325 330 335

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95      Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn
96              340              345              350
97      Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met
98              355              360              365
99      Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln
100             370              375              380
101      Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr
102             385              390              395              400
103      Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr
104              405              410              415
105      Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe
106              420              425              430
107      Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala
108              435              440              445
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 1281
112 <212> TYPE: DNA
113 <213> ORGANISM: Euglena gracilis
114 <400> SEQUENCE: 3
115      atttttttttc gaaatgaagt caaagcgcca agcgcttccc cttacaattg atggaacaac      60
116      atatgatgtg tctgcctggg tcaatttcca ccttggtggt gcggaatta tagagaatta      120
117      ccaaggaagg gatgccactg atgccttcat gggtatgcac tctcaagaag ccttcgacaa      180
118      gctcaagcgc atgccccaaa tcaatcccag ttctgagttg ccaccccagg ctgcagtga      240
119      tgaagctcaa gaggatttcc ggaagctccg agaagagttg atcgcaactg gcatgtttga      300
120      tgcttcccc ctctgtact catacaaaat cagcaccaca ctgggccttg gagtgtctgg      360
121      ttatttctctg atggttcagt atcagatgta ttctattggg gcagtgttgc ttgggatgca      420
122      ctatcaacag atgggctggc tttctcatga catttgccac caccagactt tcaagaaccg      480
123      gaactggaac aacctcgtgg gactgggtatt tggcaatggt ctgcaagggt tttccgtgac      540
124      atggtggaag gacagacaca atgcacatca ttcggaacc aatgttcaag ggcacgaccc      600
125      tgatattgac aacctcccc tcttagcctg gtctgaggat gacgtcacac gggcgtcacc      660
126      gatttccgcg aagctcattc agttccagca gtattatttc ttggtcatct gtatcttgtt      720
127      gcggttcatt tgggtgttcc agagcgtggt gaccgtgcgc agtctgaagg acagagataa      780
128      ccaattctat cgtctcagt ataagaagga ggccattggc ctgcacctgc attggacatt      840
129      gaaggccctg ttccacttat tctttatgcc cagcaccctc acatcgctgt tggatatttt      900
130      cgtttcggag ctggttggcg gcttcggcat tgcgacgtg gtgttcatga accactaccc      960
131      actggagaag atcggggact cggctcggga tggccatgga ttctcggtt gccagatcca      1020
132      tgagaccatg aacattcggc gagggattat cacagattgg ttttccggag gcttgaacta      1080
133      ccagatcgag caccatttgt ggccgacct cctcgccac aacctgacag cggtagacta      1140
134      ccaggtggaa cagctgtgcc agaagcaca cctgcggtat cggaaccgcg tgccccatga      1200
135      agggttggtc atctgtctgc gctatctggc ggtgttcgcc cggatggcgg agaagcaacc      1260
136      cgccgggaag gctctataag g                                1281
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 421
140 <212> TYPE: PRT
141 <213> ORGANISM: Euglena gracilis
142 <400> SEQUENCE: 4
143      Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
144      1              5              10              15
145      Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile

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146				20				25					30			
147	Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met
148			35					40					45			
149	His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn
150		50					55					60				
151	Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu
152	65					70					75					80
153	Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp
154				85						90					95	
155	Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu
156			100						105					110		
157	Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile
158			115					120					125			
159	Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser
160		130					135					140				
161	His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn
162	145					150					155					160
163	Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr
164				165						170					175	
165	Trp	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln
166			180					185						190		
167	Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu
168			195					200					205			
169	Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe
170		210					215					220				
171	Gln	Gln	Tyr	Tyr	Phe	Leu	Val	Ile	Cys	Ile	Leu	Leu	Arg	Phe	Ile	Trp
172	225					230					235					240
173	Cys	Phe	Gln	Ser	Val	Leu	Thr	Val	Arg	Ser	Leu	Lys	Asp	Arg	Asp	Asn
174				245						250				255		
175	Gln	Phe	Tyr	Arg	Ser	Gln	Tyr	Lys	Lys	Glu	Ala	Ile	Gly	Leu	Ala	Leu
176			260					265					270			
177	His	Trp	Thr	Leu	Lys	Ala	Leu	Phe	His	Leu	Phe	Phe	Met	Pro	Ser	Ile
178			275					280					285			
179	Leu	Thr	Ser	Leu	Leu	Val	Phe	Phe	Val	Ser	Glu	Leu	Val	Gly	Gly	Phe
180		290					295					300				
181	Gly	Ile	Ala	Ile	Val	Val	Phe	Met	Asn	His	Tyr	Pro	Leu	Glu	Lys	Ile
182	305					310					315					320
183	Gly	Asp	Ser	Val	Trp	Asp	Gly	His	Gly	Phe	Ser	Val	Gly	Gln	Ile	His
184				325						330					335	
185	Glu	Thr	Met	Asn	Ile	Arg	Arg	Gly	Ile	Ile	Thr	Asp	Trp	Phe	Phe	Gly
186			340													

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195      Ala Gly Lys Ala Leu
196      420
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 27
200 <212> TYPE: DNA
201 <213> ORGANISM: artificial sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: PCR Primer
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (12)..(12)
207 <223> OTHER INFORMATION: n = a, t, g, or c
208 <400> SEQUENCE: 5
W--> 209      ggctggctga cncaygartt ytgycay      27
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 30
213 <212> TYPE: DNA
214 <213> ORGANISM: artificial sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: PCR Primer
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (13)..(13)
220 <223> OTHER INFORMATION: n = a, t, g, or c
221 <400> SEQUENCE: 6
W--> 222      catcggttga aanarrtgrt gytcdatytg      30
224 <210> SEQ ID NO: 7
225 <211> LENGTH: 41
226 <212> TYPE: DNA
227 <213> ORGANISM: artificial sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 7
231      cccgggaagc ttctcgagga attttcaatc ctccttgggt c      41
233 <210> SEQ ID NO: 8
234 <211> LENGTH: 34
235 <212> TYPE: DNA
236 <213> ORGANISM: artificial sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: PCR Primer
239 <400> SEQUENCE: 8
240      cccgggtgga tccggaacat atcacacgaa acag      34
242 <210> SEQ ID NO: 9
243 <211> LENGTH: 6
244 <212> TYPE: RNA
245 <213> ORGANISM: artificial sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Consensus sequence
248 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/08/2004  
PATENT APPLICATION:    US/09/857,583B      TIME: 12:37:14

Input Set : N:\Crf4\Refhold\09\_folder\I857583B.raw  
Output Set: N:\CRF4\09082004\I857583B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 12  
Seq#:6; N Pos. 13  
Seq#:12; Xaa Pos. 2,3  
Seq#:13; Xaa Pos. 2,3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

**VERIFICATION SUMMARY**

DATE: 09/08/2004

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Input Set : N:\Crf4\Refhold\09\_folder\I857583B.raw

Output Set: N:\CRF4\09082004\I857583B.raw

L:8 M:270 C: Current Application Number differs, Wrong Format

L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0